

Tutorial introducing the R package simdynet

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1 Introduction

The R package simdynet provides functions to simulate realistic sexual networks. If you have not already done so, you can install simdynet using the following R command:

```
devtools::install_github('lwhittles/simdynet')
```

You should then be able to load simdynet using:

```
library('simdynet')  
## Error in library("simdynet"):  there is no package called 'simdynet'
```

Finally, if you want to reproduce exactly the same results as the ones shown in this tutorial, you should set the seed of your random number generator to the same as ours:

```
set.seed(0)
```

Throughout this vignette we use a population of size 1000 which is too small to be realistic in most settings, but this is useful to make execution of commands fast for illustration purposes.

2 Static network simulation

We can create a static snapshot of a sexual network observed over a year using:

```
s <- sim_static_sn(N = 1000, gamma = 1.8)  
## Error in sim_static_sn(N = 1000, gamma = 1.8):  could not find function "sim_static_sn"
```

This function can take four parameters, which will be the same for the other network building functions described below:

- **N** is the size of the population, the default is **N=1e4**
- **gamma** is the exponent of the power law of the degree distribution, the default is **gamma=1.8**
- **k0** determines the proportion of individuals without any relationship, the default is **k0=0.5**
- **phi** determines the rate at which relationships are evolving, the default is **phi=N**

Let's plot the degree distribution of this network:

```
plot(s$dd,xlab = '',ylab = 'Degree distribution',log = 'xy')  
## Error in plot(s$dd, xlab = "", ylab = "Degree distribution", log = "xy"):  object 's'  
not found
```

3 Simulation of outbreak in static network

Simulation of outbreaks on static sexual networks is not recommended as it is unrealistic of the way disease and network evolve on the same time scale. This functionality is provided only for comparison with the more realistic dynamic method (cf below). To simulate an outbreak on the static network generated in the previous section, we can use:

```
s <- sim_outbreak_static_sn(sn = s)

## Error in sim_outbreak_static_sn(sn = s): could not find function "sim_outbreak_static_sn"
```

Or alternatively we can simulate both the static network and the outbreak using a single command:

```
s <- sim_outbreak_static_sn(N = 1000, gamma = 1.8)

## Error in sim_outbreak_static_sn(N = 1000, gamma = 1.8): could not find function "sim_outbreak_static_sn"
```

Let's plot the degree distribution of this network:

```
plot(s$dd,xlab = '',ylab = 'Degree distribution',log = 'xy')

## Error in plot(s$dd, xlab = "", ylab = "Degree distribution", log = "xy"): object 's' not found
```

Histogram of infection times:

```
infs=s$log_infs$time[which(s$log_infs$c1=='S'&s$log_infs$c2=='U')]

## Error in eval(expr, envir, enclos): object 's' not found

hist(infs,xlab='Time',ylab='Infections',breaks = 20, main='')

## Error in hist(infs, xlab = "Time", ylab = "Infections", breaks = 20, main = ""): object 'infs' not found
```

4 Dynamic network simulation

We can simulate a dynamic network using:

```
s <- sim_dynamic_sn(N = 1000, gamma = 1.8)

## Error in sim_dynamic_sn(N = 1000, gamma = 1.8): could not find function "sim_dynamic_sn"
```

Let's plot the degree distribution of this network:

```
plot(s$dd,xlab = '',ylab = 'Degree distribution',log = 'xy')

## Error in plot(s$dd, xlab = "", ylab = "Degree distribution", log = "xy"): object 's' not found
```

5 Simulation of outbreak in dynamic network

We can simulate a dynamic network and an outbreak simultaneously using:

```
s <- sim_dynamic_sn(N = 1000, gamma = 1.8, n_infs = 1,beta=2000)

## Error in sim_dynamic_sn(N = 1000, gamma = 1.8, n_infs = 1, beta = 2000): could not find function "sim_dynamic_sn"
```

Let's plot the degree distribution of this network:

```
plot(s$dd,xlab = '',ylab = 'Degree distribution',log = 'xy')  
## Error in plot(s$dd, xlab = "", ylab = "Degree distribution", log = "xy"): object 's'  
not found
```

Histogram of infection times:

```
infs=s$log_infs$time[which(s$log_infs$c1=='S'&s$log_infs$c2=='U')]  
## Error in eval(expr, envir, enclos): object 's' not found  
hist(infs,xlab='Time',ylab='Infections',breaks = 20, main='')  
## Error in hist(infs, xlab = "Time", ylab = "Infections", breaks = 20, main = ""): object  
'infs' not found
```